

# SEQUENCE LISTING

<110> TAKAKURA, Yoshimitsu et al.

<120> A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE SAME

<130> 0230-0157P

<140> 09/856,327

<141> 2001-05-21

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 2106

<212> DNA

<213> Lyophyllum shimeji

<220>

<221> CDS

<222> (8)..(1861)

<223>

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Ser Met Gln Ile Asn Gly Gln Ile Pro Lys Asn Ala Ile His Glu Thr  
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tac gga aac gac gga gtt gat gta ttc att gca gga tct gga ccc att 145

Tyr Gly Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro Ile  
35 40 45

gga gcg acg tat gca aag ctc tgt gtt gaa gct ggt cta cgt gtt gtg 193

Gly Ala Thr Tyr Ala Lys Leu Cys Val Glu Ala Gly Leu Arg Val Val  
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atg gtc gag atc gga gct gct gat agc ttc tac gct gtt aat gcc gaa 241

Met Val Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val Asn Ala Glu  
65 70 75

gaa gga act gca gtt ccc tac gtt cct ggc tac cac aag aag aat gaa 289

Glu Gly Thr Ala Val Pro Tyr Val Pro Gly Tyr His Lys Lys Asn Glu  
80 85 90

atc gag ttc cag aaa gat att gac cgc ttc gtc aat gta atc aag gga 337

Ile Glu Phe Gln Lys Asp Ile Asp Arg Phe Val Asn Val Ile Lys Gly  
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gcc tta caa caa gtc tct gtt cct gtc aga aac cag aac gtg cct aca 385  
Ala Leu Gln Gln Val Ser Val Pro Val Arg Asn Gln Asn Val Pro Thr  
115 120 125

ctt gat ccc gga gcc tgg agc gcg ccc cct gga agt tca gcc ata tcg 433  
Leu Asp Pro Gly Ala Trp Ser Ala Pro Pro Gly Ser Ser Ala Ile Ser  
130 135 140

aac ggt aaa aat cct cac cag cgg gaa ttc gag aac ttg tct gcg gag 481  
Asn Gly Lys Asn Pro His Gln Arg Glu Phe Glu Asn Leu Ser Ala Glu  
145 150 155

gcc gta acg cgt gga gtc ggc ggc atg agt acc cac tgg acg tgc tcc 529  
Ala Val Thr Arg Gly Val Gly Gly Met Ser Thr His Trp Thr Cys Ser  
160 165 170

acg cca cgg att cat cca ccc atg gaa agt ctc ccg ggc atc ggc cgt 577  
Thr Pro Arg Ile His Pro Pro Met Glu Ser Leu Pro Gly Ile Gly Arg  
175 180 185 190

ccg aag ctc agt aac gac ccg gca gag gac gac aaa gag tgg aac gag 625  
Pro Lys Leu Ser Asn Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu  
195 200 205

ctt tat tcc gag gcc gag cgt ctc atc ggg act tcc acc aag gaa ttc 673  
Leu Tyr Ser Glu Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe  
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gac gag tca att cgg cac acc ctt gtt ctg cgc tct ttg caa gac gcg 721  
Asp Glu Ser Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala  
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Tyr Lys Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His  
240 245 250

cgg ttg aag aac gcg ccg gaa tac gtc gaa tgg cac tca gca gaa aat 817  
Arg Leu Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn  
255 260 265 270

ctt ttc cac tct atc tac aac gat gac aag cag aag aag ctc ttt acc 865  
Leu Phe His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe Thr  
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ctg ctg acg aac cat cgc tgc aca cga ctg gcg ctt acg ggc ggg tat 913  
Leu Leu Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly Gly Tyr  
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gag aag aag att ggc gct gcc gag gtc agg aat cta ctg gcc acc agg 961  
Glu Lys Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu Ala Thr Arg  
305 310 315

aat cct agt tcg cag ctg gac agc tat atc atg gcg aag gta tat gta 1009  
Asn Pro Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala Lys Val Tyr Val  
320 325 330

ctg gcg tcg gga gcg atc ggc aac cca cag att ctc tat aac tcg ggc	1057
Leu Ala Ser Gly Ala Ile Gly Asn Pro Gln Ile Leu Tyr Asn Ser Gly	
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ttc tct ggg cta cag gtc acg cca cgc aat gac tcg ttg atc ccc aac	1105
Phe Ser Gly Leu Gln Val Thr Pro Arg Asn Asp Ser Leu Ile Pro Asn	
355 360 365	
ctg ggg agg tac atc acg gag cag ccg atg gca ttt tgc cag ata gtc	1153
Leu Gly Arg Tyr Ile Thr Glu Gln Pro Met Ala Phe Cys Gln Ile Val	
370 375 380	
ttg agg cag gaa ttc gtc gac agc gtg cgc gac gat cct tat gga ctg	1201
Leu Arg Gln Glu Phe Val Asp Ser Val Arg Asp Asp Pro Tyr Gly Leu	
385 390 395	
cca tgg tgg aaa gaa gcc gtt gct caa cat att gcc aag aac ccg aca	1249
Pro Trp Trp Lys Glu Ala Val Ala Gln His Ile Ala Lys Asn Pro Thr	
400 405 410	
gat gca ctg ccc att ccg ttc cgc gat ccg gaa ccc cag gta aca acc	1297
Asp Ala Leu Pro Ile Pro Phe Arg Asp Pro Glu Pro Gln Val Thr Thr	
415 420 425 430	
cca ttt aca gaa gaa cac ccc tgg cac acg cag att cac cgc gat gct	1345
Pro Phe Thr Glu Glu His Pro Trp His Thr Gln Ile His Arg Asp Ala	
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Phe Ser Tyr Gly Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val	
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gac ctg cgc tgg ttt ggc gca acc gac cct gaa gca aac aac ctt ttg	1441
Asp Leu Arg Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu	
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gtt ttc cag aac gat gtt caa gac ggg tac agt atg ccg cag ccg acg	1489
Val Phe Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr	
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ttc aga tat cga ccc agc act gcg tca aac gtg aga gca agg aaa atg	1537
Phe Arg Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met	
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Met Ala Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu Pro	
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Thr Ser Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His Leu Ala	
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Gly Thr Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val Ala Asp Asn	
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aac tcg ctg gtc tgg gac ttt gcc aat ctt tat gtt gca ggc aat ggc 1729  
 Asn Ser Leu Val Trp Asp Phe Ala Asn Leu Tyr Val Ala Gly Asn Gly  
 560 565 570

acc atc agg acg ggc ttc ggc gag aac ccg aca ctt acg tcg atg tgc 1777  
 Thr Ile Arg Thr Gly Phe Gly Glu Asn Pro Thr Leu Thr Ser Met Cys  
 575 580 585 590

cac gct atc aag agc gcg agg agc atc atc aat aca ctc aag ggt ggg 1825  
 His Ala Ile Lys Ser Ala Arg Ser Ile Ile Asn Thr Leu Lys Gly Gly  
 595 600 605

act gac gga aaa aat aca ggc gag cat cgc aac ctt tgaggaagga 1871  
 Thr Asp Gly Lys Asn Thr Gly Glu His Arg Asn Leu  
 610 615

gcaacagcag tgtaaacaaa cgcgtcaagt ggctacttca agttgaatgc attctgggtcc 1931

cctaccatgt tgatgtgtac gataggcggtt gaaagatttt gtgtattact gaacctgtac 1991

tttgtctgaa tagttatggc actatgattc atgtttaaaa aaaaaaaaaa aaaaaaaaaa 2051

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Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Gly Ala  
 35 40 45

Thr Tyr Ala Lys Leu Cys Val Glu Ala Gly Leu Arg Val Val Met Val  
 50 55 60

Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val Asn Ala Glu Glu Gly  
 65 70 75 80

Thr Ala Val Pro Tyr Val Pro Gly Tyr His Lys Lys Asn Glu Ile Glu  
 85 90 95

Phe Gln Lys Asp Ile Asp Arg Phe Val Asn Val Ile Lys Gly Ala Leu  
100 105 110

Gln Gln Val Ser Val Pro Val Arg Asn Gln Asn Val Pro Thr Leu Asp  
115 120 125

Pro Gly Ala Trp Ser Ala Pro Pro Gly Ser Ser Ala Ile Ser Asn Gly  
130 135 140

Lys Asn Pro His Gln Arg Glu Phe Glu Asn Leu Ser Ala Glu Ala Val  
145 150 155 160

Thr Arg Gly Val Gly Gly Met Ser Thr His Trp Thr Cys Ser Thr Pro  
165 170 175

Arg Ile His Pro Pro Met Glu Ser Leu Pro Gly Ile Gly Arg Pro Lys  
180 185 190

Leu Ser Asn Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu Leu Tyr  
195 200 205

Ser Glu Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe Asp Glu  
210 215 220

Ser Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr Lys  
225 230 235 240

Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His Arg Leu  
245 250 255

Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn Leu Phe  
260 265 270

His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe Thr Leu Leu  
275 280 285

Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly Gly Tyr Glu Lys  
290 295 300

Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu Ala Thr Arg Asn Pro  
305 310 315 320

Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala Lys Val Tyr Val Leu Ala  
325 330 335

Ser Gly Ala Ile Gly Asn Pro Gln Ile Leu Tyr Asn Ser Gly Phe Ser  
340 345 350

Gly Leu Gln Val Thr Pro Arg Asn Asp Ser Leu Ile Pro Asn Leu Gly  
355 360 365

Arg Tyr Ile Thr Glu Gln Pro Met Ala Phe Cys Gln Ile Val Leu Arg  
370 375 380

Gln Glu Phe Val Asp Ser Val Arg Asp Asp Pro Tyr Gly Leu Pro Trp  
385 390 395 400

Trp Lys Glu Ala Val Ala Gln His Ile Ala Lys Asn Pro Thr Asp Ala  
405 410 415

Leu Pro Ile Pro Phe Arg Asp Pro Glu Pro Gln Val Thr Thr Pro Phe  
420 425 430

Thr Glu Glu His Pro Trp His Thr Gln Ile His Arg Asp Ala Phe Ser  
435 440 445

Tyr Gly Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val Asp Leu  
450 455 460

Arg Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu Val Phe  
465 470 475 480

Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr Phe Arg  
485 490 495

Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met Met Ala  
500 505 510

Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu Pro Thr Ser  
515 520 525

Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His Leu Ala Gly Thr  
530 535 540

Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val Ala Asp Asn Asn Ser  
545 550 555 560

Leu Val Trp Asp Phe Ala Asn Leu Tyr Val Ala Gly Asn Gly Thr Ile  
565 570 575

Arg Thr Gly Phe Gly Glu Asn Pro Thr Leu Thr Ser Met Cys His Ala  
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595 600 605

Gly Lys Asn Thr Gly Glu His Arg Asn Leu  
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Asp Ala Tyr Lys Asp Arg Gln Arg  
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Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr  
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Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr Lys Asp Arg  
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Gln Arg

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 garttycara argayathga ymg

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*Concludes*

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23

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